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Sequence 22437.22437

CCGCTCGGGCAGATTACAGTCGTTTCCAGCCCAAGTGACCTGATCGATGCCCTCCTGAATTTATCACGATATTGTGAT	16
TTATTAGCGATGCCCCCTGTTGTGTATTACGCACACACAGTGCACACAGGCTCTGGCTCGCTCCCTCCCTCGTT	48
TCCAGTCTCGGCGAATCCACATCTCTTCAACTCTCCGCCAGGGCAGCAGGAGAGTGTGCGRATCTGGC	36
AGTGAGAGGGACGAGGAAAAAAGAAAGCCACAGAGCAACTTGAGACTCCCGCATCCCAAAAGAACACCATC	108
M G P P S L V L C L L S A T V F	16
AGCAAAAAAAGAAG ATG GGC CCC CCG AGC CTC GTG CTG TGC TTG CTG TCC GCA ACT GTG TTC	48
S L L G G S S A F L S H H R L K G R F Q	36
TCC CTG CTG GGT GGA AGC TCG GCC TTC CTG TCG CAC CAC CGC CTG AAA GGC AGG TTT CAG	108
R D R R N I R P N I I L V L T D Q D V	56
AGG GAC CGC AGG AAC ATC CGC CCC AAC ATC ATC CTG GTG CTG ACG GAC CAG GAT GTG	168
E L G S M Q V M N K T R R I M E Q G G T	76
GAG CTG GGT TCC ATG CAG GTG ATG AAC AAG ACC CGG CGC ATC ATG GAG CAG GGC GGG ACG	228
H F I N A F V T T P M C C P S R S S I L	96
CAC TTC ATC AAC GCC TTC GTG ACC ACA CCC ATG TGC TGC CCC TCA CGC TCC TCC ATC CTC	288
T G K Y V H N H N T Y T N N E N C S S P	116
ACC GGC AAG TAC GTC CAC AAC CAC AAC ACC TAC ACC AAC AAT GAG AAC TGC TCC TCG CCC	348
S W Q A Q H E S R T F A V Y L N S T G Y	136
TCC TGG CAG GCA CAG CAC GAG AGC CGC ACC TTT GCC GTG TAC CTC AAT AGC ACT GGC TAC	408

Fig. 1A

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R T A F F G K Y L N E Y N G S Y V P P G 156
 CGG ACA GCT TTC TTC GGG AAG TAT CTT AAT GAA TAC AAC GGC TCC TAC GTG CCA CCC GGC 468

W K E W V G L L K N S R F Y N Y T L C R 176
 TGG AAG GAG TGG GTC GGA CTC CTT AAA AAC TCC CGC TTT TAT AAC TAC ACG CTG TGT CGG 528

N G V K E K H G S D Y S K D Y L T D L I 196
 AAC GGG GTG AAA GAG AAG CAC GGC TCC GAC TAC TCC AAG GAT TAC CTC ACA GAC CTC ATC 588

T N D S V S F F R T S K K M Y P H R P V 216
 ACC AAT GAC AGC GTG AGC TTC TTC CGC ACG TCC AAG AAG ATG TAC CCG CAC AGG CCA GTC 648

L M V I S H A A P H G P E D S A P Q Y S 236
 CTC ATG GTC ATC AGC CAT GCA GCC CCC CAC GGC CCT GAG GAT TCA GCC CCA CAA TAT TCA 708

R L F P N A S Q H I T P S Y N Y A P N P 256
 CGC CTC TTC CCA AAC GCA TCT CAG CAC ATC ACG CCG AGC TAC AAC TAC GCG CCC AAC CCG 768

D K H W I M R Y T G P M K P I H M E F T 276
 GAC AAA CAC TGG ATC ATG CGC TAC ACG GGG CCC ATG AAG CCC ATC CAC ATG GAA TTC ACC 828

N M L Q R K R L Q T L M S V D D S M E T 296
 AAC ATG CTC CAG CGG AAG CGC TTG CAG ACC CTC ATG TCG GTG GAC TCC ATG GAG ACG 888

I Y N M L V E T G E L D N T Y I V Y T A 316
 ATT TAC AAC ATG CTG GTT GAG ACG GGC GAG CTG GAC AAC ACG TAC ATC GTA TAC ACC GCC 948

Fig. 1B

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D H G Y H I G Q F G L V K G K S M P Y E 336
 GAC CAC GGT TAC CAC ATC GGC CAG TTT GGC CTG GTG AAA GGG AAA TCC ATG CCA TAT GAG 1008

F D I R V P F Y V R G P N V E A G C L N 356
 TTT GAC ATC AGG GTC CCG TTC TAC GTG AGG GGC CCC AAC GTG GAA GCC GGC TGT CTG AAT 1068

P H I V L N I D L A P T I L D I A G L D 376
 CCC CAC ATC GTC CTC AAC ATT GAC CTG GCC CCC ACC ATC CTG GAC ATT GCA GGC CTG GAC 1128

I P A D M D G K S I L K L L D T E R P V 396
 ATA CCT GCG GAT ATG GAC GGC AAA TCC ATC CTC AAC CTG CTG GAC ACG GAG CGG CCG GTG 1188

N R F H L K K M R V W R D S F L V E R 416
 AAT CGG TTT CAC TTG AAA AAG AAG ATG AGG GTC TGG CGG GAC TCC TTC TTG GTG GAG AGA 1248

G K L L H K R D N D K V D A Q E E N F L 436
 GGC AAG CTG CTA CAC AAG AGA GAC AAT GAC AAG GTG GAC GCC CAG GAG GAG AAC TTT CTG 1308

P K Y Q R V K D L C Q R A E Y Q T A C E 456
 CCC AAG TAC CAG CGT GTG AAG GAC CTG TGT CAG CGT GCT GAG TAC CAG ACG GCG TGT GAG 1368

Q L G Q K W Q C V E D A T G K L K L H K 476
 CAG CTG GGA CAG AAG TGG CAG TGT GTG GAG GAC GCC ACG GGG AAG CTG AAG CTG CAT AAG 1428

C K G P M R L G G S R A L S N L V P K Y 496
 TGC AAG GGC CCC ATG CGG CTG GGC AGC AGA GCC CTC TCC AAC CTC GTG CCC AAG TAC 1488

Fig. 1C

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Y G Q G S E A C T C D S G D Y K L S L A 516
 TAC GGG CAG GGC ACC GAG GCC TGC ACC TGT GAC AGC GGG GAC TAC AAG CTC AGC CTG GCC 1548

G R R K K L F K K Y K A S Y V R S R S 536
 GGA CGC CGG AAA AAA CTC TTC AAG AAG AAG TAC AAG GCC AGC TAT GTC CGC AGT CGC TCC 1608

I R S V A I E V D G R V Y H V G L G D A 556
 ATC CGC TCA GTG GCC ATC GAG GTG GAC GGC AGG GTG TAC CAC GTA GGC CTG GGT GAT GCC 1668

A Q P R N L T K R H W P G A P E D Q D D 576
 GCC CAG CCC CGA AAC CTC ACC AAG CCG CAC TGG CCA GGC GCC CCT GAG GAC CAA GAT GAC 1728

K D G G D F S G T G G L P D Y S A A N P 596
 AAG GAT GGT GGG GAC TTC AGT GGC ACT GGA GGC CTT CCC GAC TAC TCA GCC GCC AAC CCC 1788

I K V T H R C Y I L E N D T V Q C D L D 616
 ATT AAA GTG ACA CAT CGG TGC TAC ATC CTA GAG AAC GAC ACA GTC CAG TGT GAC CTG GAC 1848

L Y K S L Q A W K D H K L H I D H E I E 636
 CTG TAC AAG TCC CTG CAG GCC TGG AAA GAC CAC AAC CTG CAC ATC GAC CAC GAG ATT GAA 1908

T L Q N K I K N L R E V R G H L K K R 656
 ACC CTG CAG AAC AAA ATT AAG AAC CTG AGG GAA GTC CGA GGT CAC CTG AAG AAA AAG CGG 1968

P E E C D C H K I S Y H T Q H K G R L K 676
 CCA GAA GAA TGT GAC TGT CAC AAA ATC AGC TAC CAC ACC CAG CAC AAA GGC CGC CTC AAG 2028

Fig. 1D

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H R G S L H P F R K G L Q E K D K V W 696
 CAC AGA GGC TCC AGT CTG CAT CCT TTC AGG AAG GGC CTG CAA GAG AAG GAC AAG GTG TGG 2088

L L R E Q K R K K L R K L L K R L Q N 716
 CTG TTG CGG GAG CAG AAG CGC AAG AAA CTC CGC AAG CTG CTC AAG CGC CTG CAG AAC 2148

N D T C S M P G L T C F T H D N Q H W Q 736
 AAC GAC ACG TGC AGC ATG CCA GGC CTC ACG TGC TTC ACC CAC GAC AAC AAT AAC AAT AAC 2208

T A P F W T L G P F C A C T S A N N T 756
 ACG GCG CCT TTC TGG ACA CTG GGC CCT TTC TGT GGC TGC ACC AGC GCC AAC AAT AAC AAT AAC 2268

Y W C M R T I N E T H N F L F C E F A T 776
 TAC TGG TGC ATG AGG ACC ATC AAT GAG ACT CAC AAT TTC CTC TTC TGT GAA TTT GCA ACT 2328

G F L E Y F D L N Q L H V Q L M N A V N 796
 GGC TTC CTA GAG TAC TTT GAT CTC AAC ACA GAC ACT CAC AAT TTC CAG CTG ATG AAT GCA GTG AAC 2388

T L D R D V L N Q L H V Q L M E L R S C 816
 ACA CTG GAC AGG GAT GTC CTC AAC CAG CTA CAC GTA CAG CTC ATG GAG CTG AGG AGC TGC 2448

K G Y K Q C N P R T R N M D L G L K D G 836
 AAG GGT TAC AAG CAG TGT AAC CCC CGG ACT CGA AAC ATG GAC CTG GGA CTT AAA GAT GGA 2508

G S Y E Q Y R Q F Q R R K W P E M K R P 856
 GGA AGC TAT GAG CAA TAC AGG CAG TTT CAG CGT CGA AAG TGG CCA GAA ATG AAG AGA CCT 2568

Fig. 1E

S S S K S L G Q L W E G W E G *

CGAAACACACAGAGGTGGACCTCCAAAAACATAGAGGCATCACCTGACTGCACAGCAANTCAAAAAACCATGTGGGTGATTTTCCACGACAGACCTGTGCTATTGGCCAGGAGCCCTCAGAAAGCAAGCAACGCACTCTCAGTCAACATGCACAGATTCTCGAGGATAACACGACGAGGACAGAGATAACTTCAGGAAGTCCATTTTTGCCCTGCTTTTGATTTATACCTCACCAGCTGCCTGATATCAAAAAATTCATCAAAAAATTCACACTAACCTCCCCAGAAAGTCTCAAAAGGAAAAACGAGAGACGAGCGAGACAGAGAGATTTTCTTCGAAATTTCTCCAAAGGCGAAGATCATTTGGAATTTTAAATCATAGGGGAAACAGCATCTCTGTCTTAATCTCTATTCTTTTGGTTCTCAAAAGAAAGAACTAAGRAGCAGGCACTGAGGAGAGGCTGAAACACAGTCGACAGACGTTTGTACATAGCTCAGTAGCACAAAAAGATGACATTTACCTAGCACTATAAAACCCCTGGTTGCCCTTCTTGAGAAATGCCTTT

Fig. 1F

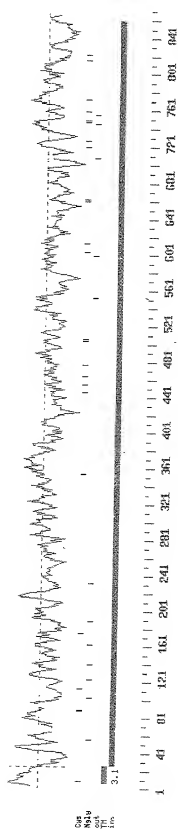


Fig. 2

22437 22437 22437

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22437 -----
1247 GAGCGAGAGTGTGTGCGAGTGTGCGTGTGTGTCGCCGCGAGGGTGCGCGCTCGGC
      10      20      30      40      50      60

22437 -----
1247 GCCGGAGCGCGGCCAGCCGAGTCCGGAGGCATCGGGAGGTCGAGACCCGCCGGGACCCC
      70      80      90      100     110     120

22437 -----
1247 AGCTCTGCGTTCACTGCCCCGTCCGGAGCTGGACTTCGGGGCGGGCGCGCGTGGC
      130     140     150     160     170     180

22437 -----
1247 CCGGGACAGGCAGGCGCGGTTCGGGGCCGCGCTCCCCCAGGCCGAGATCTGCGAGT
      190     200     210     220     230     240
    
```

Fig. 3A

Case	Year	Country	Population	Age	Gender	Occupation	Education	Income	Health	Family	Social	Environment	Policy	Impact
1	2010	USA	300M	65	M	Retired	High School	\$25K	Good	2	Low	Urban	Active	Positive
2	2012	UK	60M	55	F	Teacher	University	\$30K	Good	3	Medium	Suburban	Active	Positive
3	2015	India	1.2B	45	M	Farmer	Primary	\$10K	Fair	4	High	Rural	Passive	Negative
4	2018	Japan	125M	75	F	Homemaker	High School	\$20K	Good	1	Low	Urban	Active	Positive
5	2020	Brazil	210M	35	M	Unemployed	Primary	\$5K	Poor	5	High	Urban	Passive	Negative

[illegible]

Fig. 3B

FIG. 3C

22437	160	170	180	190	200	210
1247	ACGACGACAGGATGTGGAGCTGGGTTCCATGCAGGTGATGAACAAGACCCGGCGGCATC					
	490	500	510	520	530	540
22437	220	230	240	250	260	270
1247	ATGGACGAGGGCGGACGCACTTCATCAACGGCTTCGTGACCACACCCATGTCTGCCCC					
	550	560	570	580	590	600
22437	280	290	300	310	320	330
1247	TCACGCTCCTCCATCCTCACCGGCAAGTACGTCCACAACCAACACCTACACCAACAAT					
	610	620	630	640	650	660
22437	340	350	360	370	380	390
1247	GAGAACTGCTCCTCGGCCCTCCTGGCAGGCACAGCACGAGAGCGCGCACCTTGGCCGTGTAC					
	670	680	690	700	710	720

Fig. 3C

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22437 1247 22437 1247 22437 1247 22437 1247

22437	400	410	420	430	440	450
	CTCAATAGCACTGGCTACCGACAGCTTCTTCGGGAAGTATCTTAATGAATACACGGC					
1247	730	740	750	760	770	780
	CTCAATAGCACTGGCTACCGACAGCTTCTTCGGGAAGTATCTTAATGAATACACGGC					
22437	460	470	480	490	500	510
	TCCTACGTGCCACCGGCTGGAAGGAGTGGTCCGACTCCTTAAAACTCCCGCTTTTAT					
1247	790	800	810	820	830	840
	TCCTACGTGCCACCGGCTGGAAGGAGTGGTCCGACTCCTTAAAACTCCCGCTTTTAT					
22437	520	530	540	550	560	570
	AACTACAGCTGTGTCGGAACCGGGTGAAAGAGACGGCTCCGACTACTCCAAGGAT					
1247	850	860	870	880	890	900
	AACTACAGCTGTGTCGGAACCGGGTGAAAGAGACGGCTCCGACTACTCCAAGGAT					
22437	580	590	600	610	620	630
	TACCTCAGACGCTCATCAACAATGACAGCGTGAGCTTCTTCGCGACGTCACAAGAGATG					
1247	910	920	930	940	950	960
	TACCTCAGACGCTCATCAACAATGACAGCGTGAGCTTCTTCGCGACGTCACAAGAGATG					

Fig. 3D

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SEQUENCE

22437	640	650	660	670	680	690
1247	TACCGCACAGGCCAGTCTCATGGTTCATCAGCCATGCAGCCCCCACGGCCCTGAGGAT					
	970	980	990	1000	1010	1020
	TACCGCACAGGCCAGTCTCATGGTTCATCAGCCATGCAGCCCCCACGGCCCTGAGGAT					
22437	700	710	720	730	740	750
1247	TCAGCCCCACAATATTCACGCCCTCTCCCAACGCATCTCAGCACATCAGCCGAGCTAC					
	1030	1040	1050	1060	1070	1080
	TCAGCCCCACAATATTCACGCCCTCTCCCAACGCATCTCAGCACATCAGCCGAGCTAC					
22437	760	770	780	790	800	810
1247	AACTACGGGCCCAACCCGGACAAACACTGGATCATGGGCTACACGGGGCCCATGAAGCCC					
	1090	1100	1110	1120	1130	1140
	AACTACGGGCCCAACCCGGACAAACACTGGATCATGGGCTACACGGGGCCCATGAAGCCC					
22437	820	830	840	850	860	870
1247	ATCCACATGGAATTACCAACATGCTCCAGCGGAAGCGCTTGCAGACCCCTCATGTGCGTG					
	1150	1160	1170	1180	1190	1200
	ATCCACATGGAATTACCAACATGCTCCAGCGGAAGCGCTTGCAGACCCCTCATGTGCGTG					

Fig. 3E

22437 28224660

22437	880	890	900	910	920	930
1247	GACGACTCCATGGAGACGATTACACATGCTGTTGAGACGGCGGAGCTGGACAACACG					
	1210	1220	1230	1240	1250	1260
	1270	1280	1290	1300	1310	1320
22437	940	950	960	970	980	990
1247	TACATCGTATACACCGCCGACCGTTACACATCGGCCAGTTTGGCCTGGTGAAGGG					
	1000	1010	1020	1030	1040	1050
22437	AAATCCATGCCATATGAGTTTGACATCAGGGTCCCCTTCTACGTGAGGGGCCCAACGTG					
1247	AAATCCATGCCATATGAGTTTGACATCAGGGTCCCCTTCTACGTGAGGGGCCCAACGTG					
	1060	1070	1080	1090	1100	1110
22437	GAAGCGGCTGTCTGAATCCCACATCGTCTCAACATGACCTGGCCCCCACCATCCTG					
1247	GAAGCGGCTGTCTGAATCCCACATCGTCTCAACATGACCTGGCCCCCACCATCCTG					
	1120	1130	1140	1150	1160	1170
	1180	1190	1200	1210	1220	1230
	1240	1250	1260	1270	1280	1290
	1300	1310	1320	1330	1340	1350
	1360	1370	1380	1390	1400	1410
	1420	1430	1440	1450	1460	1470

Fig. 3F

Fig. 3G

Fig. 3G

Fig. 3H

Fig. 3I

Fig. 3J

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22437 22437 22437

22437	2020	2030	2040	2050	2060	2070
1247	CACAAAGCGCGCTCAAGACACAGAGCTCCAGTCTGCATCTTTCAGGAAGGCGCTGC					
	2350	2360	2370	2380	2390	2400
	CAAGGCGCGCTCAAGACACAGAGCTCCAGTCTGCATCTTTCAGGAAGGCGCTGC					
22437	2080	2090	2100	2110	2120	2130
1247	GAGAAAGGACAAAGGTGTGGCTGTTCGCGGAGCAGAGCGCAAGAACTCCGCAAGCTG					
	2410	2420	2430	2440	2450	2460
	GAGAAAGGACAAAGGTGTGGCTGTTCGCGGAGCAGAGCGCAAGAACTCCGCAAGCTG					
22437	2140	2150	2160	2170	2180	2190
1247	CTCAAGCGCGCTGCAGAACACGACACGTGCACATGCCAGGCTCACGTGCTTCACCCAC					
	2470	2480	2490	2500	2510	2520
	CTCAAGCGCGCTGCAGAACACGACACGTGCACATGCCAGGCTCACGTGCTTCACCCAC					
22437	2200	2210	2220	2230	2240	2250
1247	GACAAACGACACTGGCAGACGCGCGCTTCTGGACACTGGGGCTTCTGTGCCTGCACC					
	2530	2540	2550	2560	2570	2580
	GACAAACGACACTGGCAGACGCGCGCTTCTGGACACTGGGGCTTCTGTGCCTGCACC					

Fig. 3K

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SECRET 660660

22437	2260	2270	2280	2290	2300	2310
	AGGCCAACAATAACACGTACTGGTGCATGAGGACCATCAATGAGACTCACAATTTCCTC					
	2590	2600	2610	2620	2630	2640
1247	AGGCCAACAATAACACGTACTGGTGCATGAGGACCATCAATGAGACTCACAATTTCCTC					
	2320	2330	2340	2350	2360	2370
22437	TTCTGTGAATTGCAACTGGCTTCCTAGACTACTTTGATCTCAACACAGACCCCTACCAG					
	2650	2660	2670	2680	2690	2700
1247	TTCTGTGAATTGCAACTGGCTTCCTAGACTACTTTGATCTCAACACAGACCCCTACCAG					
	2380	2390	2400	2410	2420	2430
22437	CTGATGAATGCAGTGAACACACTGGACAGGGATGTCTCAACCAGCTACACGTACAGTTC					
	2710	2720	2730	2740	2750	2760
1247	CTGATGAATGCAGTGAACACACTGGACAGGGATGTCTCAACCAGCTACACGTACAGTTC					
	2440	2450	2460	2470	2480	2490
22437	ATGGAGCTGAGGAGCTGCAAGGGTTACAAGCAGTGTAAACCCCGGACTCGAAACATGGAC					
	2770	2780	2790	2800	2810	2820
1247	ATGGAGCTGAGGAGCTGCAAGGGTTACAAGCAGTGTAAACCCCGGACTCGAAACATGGAC					

Fig. 3L

Fig. 3M

22437 -----
1247 GCAGCAGCAGCTCTCAGTCAACATCACAGATCTCGAGGATAACCCAGCAGGACAGAGA
3070 3080 3090 3100 3110 3120
22437 -----
1247 TAACTTCAGGAAGTCCATTTTGGCCCTGCTTTTGGATTATACCTCACCAAGCTGC
3130 3140 3150 3160 3170 3180
22437 -----
1247 ACAAATGCATTTTTCGTATCAAAAAGTCACCACTAACCCCTCCCCGAGAAGCTCACAAA
3190 3200 3210 3220 3230 3240
22437 -----
1247 GGAAACGGAGAGAGCGAGCGAGAGAGATTTCTTGGAAATTTCTCCCAAGGGGAAAGT
3250 3260 3270 3280 3290 3300

Fig. 3N

12437 22437 22437

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22437 -----  
1247 CATTGGAATTTTAAATCATAGGGGAAAGCAGTCCTGTTCTAAATCCTTTATTTCTTTT  
3310 3320 3330 3340 3350 3360  
22437 -----  
1247 GGTTTGTCACAAAAGAGGAACTAAGAAGCAGGACAGAGGCAACCTGGAGAGGCTGAAAAAC  
3370 3380 3390 3400 3410 3420  
22437 -----  
1247 AGTGCAGAGACGTTTGACAATGAGTCAGTAGCAGACAAAAGAGATGACATTTACCTAGCACT  
3430 3440 3450 3460 3470 3480  
22437 -----  
1247 ATAAACCCTGGTTGGCTCTGAAGAAACTGCCCTTCATTGTATATATGTGACTATTTACATG  
3490 3500 3510 3520 3530 3540
```

Fig. 30

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TTCTTTTAAAGTAAATGAAGTATGTCCTGATGTTTCTCTAGTATTTCTTTGTTATGTCCAGAACTGATGTT

22437	-----	
1247	TAATCAACATGGGAACCTTTTAGGGGAACCTAATAAGAAATCCCAATTTT	CAGGAGTGGTG 3550 3560 3570 3580 3590 3600
22437	-----	
1247	GTGTCAATAAACGCTCTGTGGCCAGTGTAAAAGAAATCCCTCGCAGTTGT	GGACATTTC 3610 3620 3630 3640 3650 3660
22437	-----	
1247	TGTTCTGTCCAGATACCATTTCTCCTAGTATTTCTTTGTTATGTCCAGAACTGATGTT	3670 3680 3690 3700 3710 3720
22437	-----	
1247	TTTTTTTAAAGTACTGAAAAGAAATGAAGTTGATGTATGTCCCAAGTTT	TGATGAAACT 3730 3740 3750 3760 3770 3780

Fig. 3P

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22437 28202660

22437	-----	
1247	GTATTGTAAAAAATTTTGTAGTTTAAGTATTGTACATACAGTGTTCAAAACCCCAGCC	3790 3800 3810 3820 3830 3840
22437	-----	
1247	AATGACCAGCAGTTGGTATGAAGAACCTTTGACATTTTGTAAGGCGCATTTCTTTCTTG	3850 3860 3870 3880 3890 3900
22437	-----	
1247	GGAGTTTTTGGTGTGTCGTGTTTTTTTAAAGTATTCAAGATACTACCAGTCAACATCTTT	3910 3920 3930 3940 3950 3960
22437	-----	
1247	TTGGAAGAAAATGCCCTTGGGTTTAGAAGATTTTCTTAAAGGGGAGTAGATGGTTGTAGA	3970 3980 3990 4000 4010 4020

Fig. 3Q

FIG. 3R

22437	-----	
1247	TTGACTAAAAAGTCTACCACTACTTCAAGGGACTACAGGTAAAGTCTCATAGTATACCAAGCT	4030 4040 4050 4060 4070 4080
22437	-----	
1247	TTGGTACTTTCATTTTTTAAAAAAGTATTAAATCAATTGCAAGAAAAATTCGCCTTGGCCCAAC	4090 4100 4110 4120 4130 4140
22437	-----	
1247	CCTTCTTTGTGTATCAGGTAGTCTAACCTGATACAAAGTAGTTGACAGATTTCAACTATCA	4150 4160 4170 4180 4190 4200
22437	-----	
1247	ATCACCAGTCCAACCCATTCTCTCATTTAACAGATGACGGAGATAATCCCTAAAAGCACCC	4210 4220 4230 4240 4250 4260

Fig. 3R

22437 -----
1247 ACAATTGTTTCAATGCCCCCAACAGGCCAAGGCTCCCTAGCAACTCCCTAGTGGCGTTTT
4270 4280 4290 4300 4310 4320
22437 -----
1247 TTAACCTTCACAGAAACTGTTACCAATTATTGAAATAGGCTTCCTTAACCTCCCTTTACCT
4330 4340 4350 4360 4370 4380
22437 -----
1247 TAACCCCAACAGGGATT
4390

Fig. 3S

Fig. 4A

Fig. 4A

Sheet 28 of 66

22437	230	240	250	260	270	280	
	HPEDSAQYSRLFPNASQHITPSYNYAPNPKHWIMRYTGPMPKPIHMEFTNMLQKRRLQ						
1247	250	260	270	280	290	300	
	HPEDSAQYSRLFPNASQHITPSYNYAPNPKHWIMRYTGPMPKPIHMEFTNMLQKRRLQ						
22437	290	300	310	320	330	340	
	TLMSVDDSMETIYNMLVETGELDNITYVYTADHGYHIGQGLVKGKSMPIYEFDIRVPFYV						
1247	310	320	330	340	350	360	
	TLMSVDDSMETIYNMLVETGELDNITYVYTADHGYHIGQGLVKGKSMPIYEFDIRVPFYV						
22437	350	360	370	380	390	400	
	RGPVVEAGCINPHIVLINIDLAPTILDIAGLDIPADMWGKSIKLLDTERPVPVNRFHLKKKM						
1247	370	380	390	400	410	420	
	RGPVVEAGCINPHIVLINIDLAPTILDIAGLDIPADMWGKSIKLLDTERPVPVNRFHLKKKM						
22437	410	420	430	440	450	460	
	RVWRDSFLVERGKLLHKRNDKVDQAEENFLPKYQRVKDLQRAEYQTACEQLGQKWQCV						
1247	430	440	450	460	470	480	
	RVWRDSFLVERGKLLHKRNDKVDQAEENFLPKYQRVKDLQRAEYQTACEQLGQKWQCV						

Fig. 4B

[illegible]

Fig. 4C

SEQUENCE LISTING

22437	710	720	730	740	750	760	770	780
	KLRKLLKRLQNNDTC	SMPGLTCFTHDNQHWQTAPFWTLGPFCACT	SANNNTYWC	MRTINE				
1247	730	740	750	760	770	780		
	KLRKLLKRLQNNDTC	SMPGLTCFTHDNQHWQTAPFWTLGPFCACT	SANNNTYWC	MRTINE				
22437	770	780	790	800	810	820		
	THNLFCE	FATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQLHVQLMELRSCKGYKQC	NPR					
1247	790	800	810	820	830	840		
	THNLFCE	FATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQLHVQLMELRSCKGYKQC	NPR					
22437	830	840	850	860	870			
	TRNMDLGLKDGGSYE	QYRQFQRRKWP	EMKRPSSKSLGQLWEG	WEG				
1247	850	860	870	880				
	TRNMDLGLKDGGSYE	QYRQFQRRKWP	EMKRPSSKSLGQLWEG	WEG				

Fig. 4D